

CAGCCCTCAT CTCCGCCGGC GAGTAGGGCC AGGTGTTGGG AGCTCCCACG TGGGACAAGG 60
 TGGTGTCTTC GGCGCAG 77

atg ggt ttc aac ctg cag gct ctc ctg gag cag ctc agc cag gat gag 125
 Met Gly Phe Asn Leu Gln Ala Leu Leu Glu Gln Leu Ser Gln Asp Glu
 1 5 10 15

ttg agc aag ttc aag tat ctg atc acg acc ttc tcc ccg gca cac gag 173
 Leu Ser Lys Phe Lys Tyr Leu Ile Thr Thr Phe Ser Pro Ala His Glu
 20 25 30

ctc cag aag atc ccc cac aag gag gta gac aag gct gat ggg aag caa 221
 Leu Gln Lys Ile Pro His Lys Glu Val Asp Lys Ala Asp Gly Lys Gln
 35 40 45

ctg gta gaa atc ctc acc acc cat tgt gac agc tac tgg gtg gag atg 269
 Leu Val Glu Ile Leu Thr Thr His Cys Asp Ser Tyr Trp Val Glu Met
 50 55 60

gcg agc ctc cag gtc ttt gaa aag atg cac cga atg gat ctg tct gag 317
 Ala Ser Leu Gln Val Phe Glu Lys Met His Arg Met Asp Leu Ser Glu
 65 70 75 80

aga gca aag gat gaa gtc aga gaa gca gct ttg aaa tcc ttt aat aaa 365
 Arg Ala Lys Asp Glu Val Arg Glu Ala Ala Leu Lys Ser Phe Asn Lys
 85 90 95

agg aag cct cta tca tta ggg ata aca cgg aaa gaa cga cca cct cta 413
 Arg Lys Pro Leu Ser Leu Gly Ile Thr Arg Lys Glu Arg Pro Pro Leu
 100 105 110

gac gtg gac gaa atg ctg gag cgc ttc aaa aca gaa gca caa gac aaa 461
 Asp Val Asp Glu Met Leu Glu Arg Phe Lys Thr Glu Ala Gln Asp Lys
 115 120 125

gac aat agg tgc agg tat ata ttg aag acg aag ttc cgg gag atg tgg 509
 Asp Asn Arg Cys Arg Tyr Ile Leu Lys Thr Lys Phe Arg Glu Met Trp
 130 135 140

aag agc tgg cct gga gat agc aaa gag gtc cag gtt atg gct gag aga 557
 Lys Ser Trp Pro Gly Asp Ser Lys Glu Val Gln Val Met Ala Glu Arg
 145 150 155 160

tac aag atg ctg atc cca ttt agc aac ccc agg gtg ctt ccc ggg ccc 605
 Tyr Lys Met Leu Ile Pro Phe Ser Asn Pro Arg Val Leu Pro Gly Pro
 165 170 175

ttc tca tac acg gtg gtg ctg tat ggt cct gca ggc ctt ggg aaa acc 653
 Phe Ser Tyr Thr Val Val Leu Tyr Gly Pro Ala Gly Leu Gly Lys Thr
 180 185 190

acg ctg gcc cag aaa cta atg cta gac tgg gca gag gac aac ctc atc 701
 Thr Leu Ala Gln Lys Leu Met Leu Asp Trp Ala Glu Asp Asn Leu Ile
 195 200 205

FIG. 1A

cac	aaa	ttc	aaa	tat	gcg	ttc	tac	ctc	agc	tgc	agg	gag	ctc	agc	cgc	749
His	Lys	Phe	Lys	Tyr	Ala	Phe	Tyr	Leu	Ser	Cys	Arg	Glu	Leu	Ser	Arg	
	210					215					220					
ctg	ggc	ccg	tgc	agt	ttt	gca	gag	ctg	gtc	ttc	agg	gac	tgg	cct	gaa	797
Leu	Gly	Pro	Cys	Ser	Phe	Ala	Glu	Leu	Val	Phe	Arg	Asp	Trp	Pro	Glu	
225					230					235					240	
ttg	cag	gat	gac	att	cca	cac	atc	cta	gcc	caa	gca	cgg	aaa	atc	ttg	845
Leu	Gln	Asp	Asp	Ile	Pro	His	Ile	Leu	Ala	Gln	Ala	Arg	Lys	Ile	Leu	
				245					250					255		
ttc	gtg	att	gac	ggc	ttt	gat	gag	ctg	gga	gcc	gca	cct	ggg	gcg	ctg	893
Phe	Val	Ile	Asp	Gly	Phe	Asp	Glu	Leu	Gly	Ala	Ala	Pro	Gly	Ala	Leu	
			260					265					270			
atc	gag	gac	atc	tgc	ggg	gac	tgg	gag	aag	aag	aag	ccg	gtg	ccc	gtc	941
Ile	Glu	Asp	Ile	Cys	Gly	Asp	Trp	Glu	Lys	Lys	Lys	Pro	Val	Pro	Val	
		275					280					285				
ctc	ctg	ggg	agt	ttg	ctg	aac	agg	gtg	atg	tta	ccc	aag	gcc	gcc	ctg	989
Leu	Leu	Gly	Ser	Leu	Leu	Asn	Arg	Val	Met	Leu	Pro	Lys	Ala	Ala	Leu	
	290					295					300					
ctg	gtc	acc	acg	cgg	ccc	agg	gcc	ctg	agg	gac	ctc	cgg	atc	ctg	gcg	1037
Leu	Val	Thr	Thr	Arg	Pro	Arg	Ala	Leu	Arg	Asp	Leu	Arg	Ile	Leu	Ala	
305					310					315					320	
gag	gag	ccg	atc	tac	ata	agg	gtg	gag	ggc	ttc	ctg	gag	gag	gac	aag	1085
Glu	Glu	Pro	Ile	Tyr	Ile	Arg	Val	Glu	Gly	Phe	Leu	Glu	Glu	Asp	Lys	
				325					330					335		
agg	gcc	tat	ttc	ctg	aga	cac	ttt	gga	gac	gag	gac	caa	gcc	atg	cgt	1133
Arg	Ala	Tyr	Phe	Leu	Arg	His	Phe	Gly	Asp	Glu	Asp	Gln	Ala	Met	Arg	
			340					345					350			
gcc	ttt	gag	cta	atg	agg	agc	aac	gcg	gcc	ctg	ttc	cag	ctg	ggc	tgc	1181
Ala	Phe	Glu	Leu	Met	Arg	Ser	Asn	Ala	Ala	Leu	Phe	Gln	Leu	Gly	Ser	
		355					360					365				
gcc	ccc	gcg	gtg	tgc	tgg	atc	gtg	tgc	acg	act	ctg	aag	ctg	cag	atg	1229
Ala	Pro	Ala	Val	Cys	Trp	Ile	Val	Cys	Thr	Thr	Leu	Lys	Leu	Gln	Met	
	370					375					380					
gag	aag	ggg	gag	gac	ccg	gtc	ccc	acc	tgc	ctc	acc	cgc	acg	ggg	ctg	1277
Glu	Lys	Gly	Glu	Asp	Pro	Val	Pro	Thr	Cys	Leu	Thr	Arg	Thr	Gly	Leu	
385					390					395					400	
ttc	ctg	cgt	ttc	ctc	tgc	agc	cgg	ttc	ccg	cag	ggc	gca	cag	ctg	cgg	1325
Phe	Leu	Arg	Phe	Leu	Cys	Ser	Arg	Phe	Pro	Gln	Gly	Ala	Gln	Leu	Arg	
				405					410					415		
ggc	gcg	ctg	cgg	acg	ctg	agc	ctc	ctg	gcc	gcg	cag	ggc	ctg	tgg	gcg	1373
Gly	Ala	Leu	Arg	Thr	Leu	Ser	Leu	Leu	Ala	Ala	Gln	Gly	Leu	Trp	Ala	
			420					425					430			

FIG. 1B

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF

cag	acg	tcc	gtg	ctt	cac	cga	gag	gat	ctg	gaa	agg	ctc	ggg	gtg	cag	1421
Gln	Thr	Ser	Val	Leu	His	Arg	Glu	Asp	Leu	Glu	Arg	Leu	Gly	Val	Gln	
		435					440					445				
gag	tcc	gac	ctc	cgt	ctg	ttc	ctg	gac	gga	gac	atc	ctc	cgc	cag	gac	1469
Glu	Ser	Asp	Leu	Arg	Leu	Phe	Leu	Asp	Gly	Asp	Ile	Leu	Arg	Gln	Asp	
	450					455					460					
aga	gtc	tcc	aaa	ggc	tgc	tac	tcc	ttc	atc	cac	ctc	agc	ttc	cag	cag	1517
Arg	Val	Ser	Lys	Gly	Cys	Tyr	Ser	Phe	Ile	His	Leu	Ser	Phe	Gln	Gln	
465					470					475					480	
ttt	ctc	act	gcc	ctg	ttc	tac	acc	ctg	gag	aag	gag	gag	gaa	gag	gat	1565
Phe	Leu	Thr	Ala	Leu	Phe	Tyr	Thr	Leu	Glu	Lys	Glu	Glu	Glu	Glu	Asp	
				485					490						495	
agg	gac	ggc	cac	acc	tgg	gac	att	ggg	gac	gta	cag	aag	ctg	ctt	tcc	1613
Arg	Asp	Gly	His	Thr	Trp	Asp	Ile	Gly	Asp	Val	Gln	Lys	Leu	Leu	Ser	
			500					505					510			
gga	gta	gaa	aga	ctc	agg	aac	ccc	gac	ctg	atc	caa	gca	ggc	tac	tac	1661
Gly	Val	Glu	Arg	Leu	Arg	Asn	Pro	Asp	Leu	Ile	Gln	Ala	Gly	Tyr	Tyr	
		515					520					525				
tcc	ttt	ggc	ctc	gct	aac	gag	aag	aga	gcc	aag	gag	ttg	gag	gcc	act	1709
Ser	Phe	Gly	Leu	Ala	Asn	Glu	Lys	Arg	Ala	Lys	Glu	Leu	Glu	Ala	Thr	
	530					535					540					
ttt	ggc	tgc	cgg	atg	tca	ccg	gac	atc	aaa	cag	gaa	ttg	ctg	cga	tgc	1757
Phe	Gly	Cys	Arg	Met	Ser	Pro	Asp	Ile	Lys	Gln	Glu	Leu	Leu	Arg	Cys	
545					550					555					560	
gac	ata	agt	tgt	aag	ggt	gga	cat	tca	acg	gtg	aca	gac	ctg	cag	gag	1805
Asp	Ile	Ser	Cys	Lys	Gly	Gly	His	Ser	Thr	Val	Thr	Asp	Leu	Gln	Glu	
				565					570						575	
ctc	ctc	ggc	tgt	ctg	tac	gag	tct	cag	gag	gag	gag	ctg	gtg	aag	gag	1853
Leu	Leu	Gly	Cys	Leu	Tyr	Glu	Ser	Gln	Glu	Glu	Glu	Leu	Val	Lys	Glu	
			580					585					590			
gtg	atg	gct	cag	ttc	aaa	gaa	ata	tcc	ctg	cac	tta	aat	gca	gta	gac	1901
Val	Met	Ala	Gln	Phe	Lys	Glu	Ile	Ser	Leu	His	Leu	Asn	Ala	Val	Asp	
		595					600					605				
gtt	gtg	cca	tct	tca	ttc	tgc	gtc	aag	cac	tgt	cga	aac	ctg	cag	aaa	1949
Val	Val	Pro	Ser	Ser	Phe	Cys	Val	Lys	His	Cys	Arg	Asn	Leu	Gln	Lys	
	610					615					620					
atg	tca	ctg	cag	gta	ata	aag	gag	aat	ctc	ccg	gag	aat	gtc	act	gcg	1997
Met	Ser	Leu	Gln	Val	Ile	Lys	Glu	Asn	Leu	Pro	Glu	Asn	Val	Thr	Ala	
625					630					6						

FIG. 1C

ctt	cct	ttc	tgg	acg	gac	ctt	tgt	tcc	ata	ttt	gga	tca	aat	aag	gat	2093
Leu	Pro	Phe	Trp	Thr	Asp	Leu	Cys	Ser	Ile	Phe	Gly	Ser	Asn	Lys	Asp	
			660					665					670			
ctg	atg	ggg	cta	gca	atc	aat	gat	agc	ttt	ctc	agt	gcc	tcc	cta	gta	2141
Leu	Met	Gly	Leu	Ala	Ile	Asn	Asp	Ser	Phe	Leu	Ser	Ala	Ser	Leu	Val	
		675					680					685				
agg	atc	ctg	tgt	gaa	caa	ata	gcc	tct	gac	acc	tgt	cat	ctc	cag	aga	2189
Arg	Ile	Leu	Cys	Glu	Gln	Ile	Ala	Ser	Asp	Thr	Cys	His	Leu	Gln	Arg	
	690					695					700					
gtg	gtg	ttc	aaa	aac	att	tcc	cca	gct	gat	gct	cat	cgg	aac	ctc	tgc	2237
Val	Val	Phe	Lys	Asn	Ile	Ser	Pro	Ala	Asp	Ala	His	Arg	Asn	Leu	Cys	
705					710					715					720	
cta	gct	ctt	cga	ggg	cac	aag	act	gta	acg	tat	ctg	acc	ctt	caa	ggc	2285
Leu	Ala	Leu	Arg	Gly	His	Lys	Thr	Val	Thr	Tyr	Leu	Thr	Leu	Gln	Gly	
				725					730					735		
aat	gac	cag	gat	gat	atg	ttt	ccc	gca	ttg	tgt	gag	gtc	ttg	aga	cat	2333
Asn	Asp	Gln	Asp	Asp	Met	Phe	Pro	Ala	Leu	Cys	Glu	Val	Leu	Arg	His	
			740					745					750			
cca	gaa	tgt	aac	ctg	cga	tat	ctc	ggg	ttg	gtg	tct	tgt	tcc	gct	acc	2381
Pro	Glu	Cys	Asn	Leu	Arg	Tyr	Leu	Gly	Leu	Val	Ser	Cys	Ser	Ala	Thr	
		755					760					765				
act	cag	cag	tgg	gct	gat	ctc	tcc	ttg	gcc	ctt	gaa	gtc	aac	cag	tcc	2429
Thr	Gln	Gln	Trp	Ala	Asp	Leu	Ser	Leu	Ala	Leu	Glu	Val	Asn	Gln	Ser	
	770					775					780					
ctg	acg	tgc	gta	aac	ctc	tcc	gac	aat	gag	ctt	ctg	gat	gag	ggg	gct	2477
Leu	Thr	Cys	Val	Asn	Leu	Ser	Asp	Asn	Glu	Leu	Leu	Asp	Glu	Gly	Ala	
785					790				795						800	
aag	ttg	ctg	tac	aca	act	ttg	aga	cac	ccc	aag	tgc	ttt	ctg	cag	agg	2525
Lys	Leu	Leu	Tyr	Thr	Thr	Leu	Arg	His	Pro	Lys	Cys	Phe	Leu	Gln	Arg	
				805					810					815		
ttg	tcg	ttg	gaa	aac	tgt	cac	ctt	aca	gaa	gcc	aat	tgc	aag	gac	ctt	2573
Leu	Ser	Leu	Glu	Asn	Cys	His	Leu	Thr	Glu	Ala	Asn	Cys	Lys	Asp	Leu	
			820					825					830			
gct	gct	gtg	ttg	gtt	gtc	agc	cgg	gag	ctg	aca	cac	ctg	tgc	ttg	gcc	2621
Ala	Ala	Val	Leu	Val	Val	Ser	Arg	Glu	Leu	Thr	His	Leu	Cys	Leu	Ala	
		835					840					845				
aag	aac	ccc	att	ggg	aat	aca	ggg	gtg	aag	ttt	ctg	tgt	gag	ggc	ttg	2669
Lys	Asn	Pro	Ile	Gly	Asn	Thr	Gly	Val	Lys	Phe	Leu	Cys	Glu	Gly	Leu	
	850					855					860					
agg	tac	ccc	gag	tgt	aaa	ctg	cag	acc	ttg	gtg	ctt	tgg	aac	tgc	gac	2717
Arg	Tyr	Pro	Glu	Cys	Lys	Leu	Gln	Thr	Leu	Val	Leu	Trp	Asn	Cys	Asp	
865					870				875						880	

FIG. 1D

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Applicant(s): John Bertin et al.

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

ata act agc gat ggc tgc tgc gat ctc aca aag ctt ctc caa gaa aaa	2765
ile Thr Ser Asp Gly Cys Cys Asp Leu Thr Lys Leu Leu Gln Glu Lys	
885 890 895	
tca agc ctg ttg tgt ttg gat ctg ggg ctg aat cac ata gga gtt aag	2813
Ser Ser Leu Leu Cys Leu Asp Leu Gly Leu Asn His Ile Gly Val Lys	
900 905 910	
gga atg aag ttc ctg tgt gag gct ttg agg aaa cca ctg tgc aac ttg	2861
Gly Met Lys Phe Leu Cys Glu Ala Leu Arg Lys Pro Leu Cys Asn Leu	
915 920 925	
aga tgt ctg tgg ttg tgg gga tgt tcc atc cct ccg ttc agt tgt gaa	2909
Arg Cys Leu Trp Leu Trp Gly Cys Ser Ile Pro Pro Phe Ser Cys Glu	
930 935 940	
gac ctc tgc tct gcc ctc agc aac cag agc ctc gtc act ctg gac ctg	2957
Asp Leu Cys Ser Ala Leu Ser Asn Gln Ser Leu Val Thr Leu Asp Leu	
945 950 955 960	
ggt cag aat ccc ttg ggg tct agt gga gtg aag atg ctg ttt gaa acc	3005
Gly Gln Asn Pro Leu Gly Ser Ser Gly Val Lys Met Leu Phe Glu Thr	
965 970 975	
ttg aca tgt tcc agt ggc acc ctc cgg aca ctc agg ttg aaa atc gat	3053
Leu Thr Cys Ser Ser Gly Thr Leu Arg Thr Leu Arg Leu Lys Ile Asp	
980 985 990	
gac ttt aat gat gaa ctc aat aag ctg ctg gaa gaa ata gaa gaa aaa	3101
Asp Phe Asn Asp Glu Leu Asn Lys Leu Leu Glu Glu Ile Glu Glu Lys	
995 1000 1005	
aac cca caa ctg att att gat act gag aaa cat cat ccc tgg gca gaa	3149
Asn Pro Gln Leu Ile Ile Asp Thr Glu Lys His His Pro Trp Ala Glu	
1010 1015 1020	
agg cct tct tct cat gac ttc atg atc	3176
Arg Pro Ser Ser His Asp Phe Met Ile	
1025 1030	
TGAATCCCCC CGAGTCATTC ATTCTCCATG AAGTCATCGA TTTTCCAGGT GTTGGTGAAC	3236
TGCCTGTGAC TCCTCTCCTC CCCGGCCCCCT ACCCCTCAGG GATAATGAGT TCATTGCTGG	3296
GCTAGATGTT TTAGCCATGA TTCTGCCTCT GTTTTATACC TGCACACATC CTTATCTTTG	3356
TTACATATGA AATATCTGTA TCACGGGTAT ATTGAGAGAA ATAAAGGTGA GAGCATTCAC	3416
AAAAAAAAAA AAAAA	3431

FIG. 1E

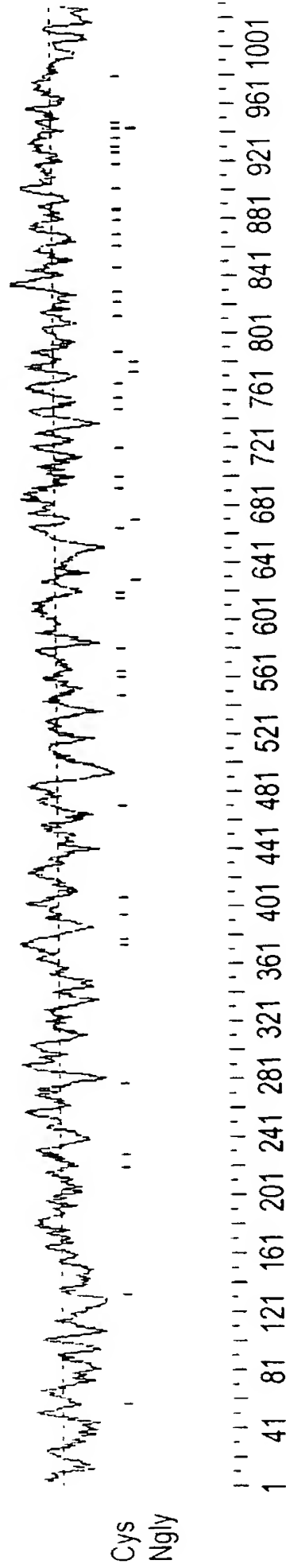
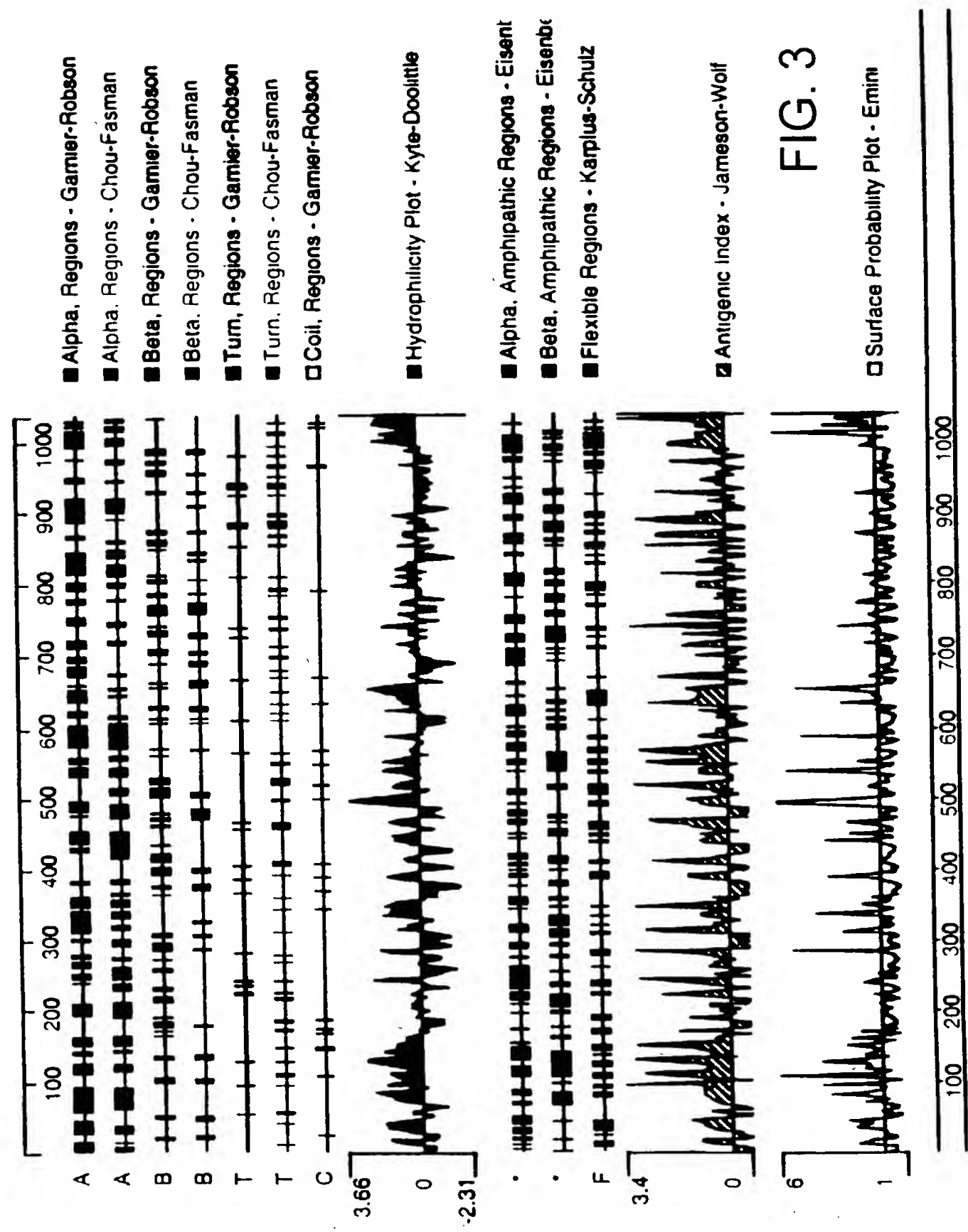


FIG. 2



NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

ccacgcgtcc gccacgcgt cggggcatct ggggaaacct ttcttccatg gctcaggaca	60
cactcctgga tcgagccaac aggagaactt tctgtgtgga ccgaagccta aggaccctga	120
aaacagctgc agatgaag atg gca agc acc cgc tgc aag ctg gcc agg tac	171
Met Ala Ser Thr Arg Cys Lys Leu Ala Arg Tyr	
1 5 10	
ctg gag gac ctg gag gat gtg gac ttg aag aaa ttt aag atg cac tta	219
Leu Glu Asp Leu Glu Asp Val Asp Leu Lys Lys Phe Lys Met His Leu	
15 20 25	
gag gac tat cct ccc cag aag ggc tgc atc ccc ctc ccg agg ggt cag	267
Glu Asp Tyr Pro Pro Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gln	
30 35 40	
aca gag aag gca gac cat gtg gat cta gcc acg cta atg atc gac ttc	315
Thr Glu Lys Ala Asp His Val Asp Leu Ala Thr Leu Met Ile Asp Phe	
45 50 55	
aat ggg gag gag aag gcg tgg gcc atg gcc gtg tgg atc ttc gct gcg	363
Asn Gly Glu Glu Lys Ala Trp Ala Met Ala Val Trp Ile Phe Ala Ala	
60 65 70 75	
atc aac agg aga gac ctt tat gag aaa gca aaa aga gat gag ccg aag	411
Ile Asn Arg Arg Asp Leu Tyr Glu Lys Ala Lys Arg Asp Glu Pro Lys	
80 85 90	
tgg ggt tca gat aat gca cgt gtt tcg aat ccc act gtg ata tgc cag	459
Trp Gly Ser Asp Asn Ala Arg Val Ser Asn Pro Thr Val Ile Cys Gln	
95 100 105	
gaa gac agc att gaa gag gag tgg atg ggt tta ctg gag tac ctt tcg	507
Glu Asp Ser Ile Glu Glu Glu Trp Met Gly Leu Leu Glu Tyr Leu Ser	
110 115 120	
aga atc tct att tgt aaa atg aag aaa gat tac cgt aag aag tac aga	555
Arg Ile Ser Ile Cys Lys Met Lys Lys Asp Tyr Arg Lys Lys Tyr Arg	
125 130 135	
aag tac gtg aga agc aga ttc cag tgc att gaa gac agg aat gcc cgt	603
Lys Tyr Val Arg Ser Arg Phe Gln Cys Ile Glu Asp Arg Asn Ala Arg	
140 145 150 155	
ctg ggt gag agt gtg agc ctc aac aaa cgc tac aca cga ctg cgt ctc	651
Leu Gly Glu Ser Val Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg Leu	
160 165 170	
atc aag gag cac cgg agc cag cag gag agg gag cag gag ctt ctg gcc	699
Ile Lys Glu His Arg Ser Gln Gln Glu Arg Glu Gln Glu Leu Leu Ala	
175 180 185	
atc ggc aag acc aag acg tgt gag agc ccc gtg agt ccc att aag atg	747
Ile Gly Lys Thr Lys Thr Cys Glu Ser Pro Val Ser Pro Ile Lys Met	
190 195 200	
gag ctg ctg ttt gac ccc gat gat gag cat tct gag cct gtg cac acc	795
Glu Leu Leu Phe Asp Pro Asp Asp Glu His Ser Glu Pro Val His Thr	
205 210 215	

FIG. 4A

gtg gtg ttc cag ggg gcg gca ggg att ggg aaa aca atc ctg gcc agg Val Val Phe Gln Gly Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala Arg 220 225 230 235	843
aag atg atg ttg gac tgg gca tgg ggg aca ctc tac caa gac agg ttt Lys Met Met Leu Asp Trp Ala Ser Gly Thr Leu Tyr Gln Asp Arg Phe 240 245 250	891
gac tat ctg ttc tat atc cac tgt cgg gag gtg agc ctt gtg aca cag Asp Tyr Leu Phe Tyr Ile His Cys Arg Glu Val Ser Leu Val Thr Gln 255 260 265	939
agg agc ctg ggg gac ctg atc atg agc tgc tgc ccc gac cca aac cca Arg Ser Leu Gly Asp Leu Ile Met Ser Cys Cys Pro Asp Pro Asn Pro 270 275 280	987
ccc atc cac aag atc gtg aga aaa ccc tcc aga atc ctc ttc ctc atg Pro Ile His Lys Ile Val Arg Lys Pro Ser Arg Ile Leu Phe Leu Met 285 290 295	1035
gac ggc ttc gat gag ctg caa ggt gcc ttt gac gag cac ata gga ccg Asp Gly Phe Asp Glu Leu Gln Gly Ala Phe Asp Glu His Ile Gly Pro 300 305 310 315	1083
ctc tgc act gac tgg cag aag gcc gag cgg gga gac att ctc ctg agc Leu Cys Thr Asp Trp Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu Ser 320 325 330	1131
agc ctc atc aga aag aag ctg ctt ccc gag gcc tct ctg ctc atc acc Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile Thr 335 340 345	1179
acg aga cct gtg gcc ctg gag aaa ctg cag cac ttg ctg gac cat cct Thr Arg Pro Val Ala Leu Glu Lys Leu Gln His Leu Leu Asp His Pro 350 355 360	1227
cgg cat gtg gag atc ctg ggt ttc tcc gag gcc aaa agg aaa gag tac Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu Tyr 365 370 375	1275
ttc ttc aag tac ttc tct gat gag gcc caa gcc agg gca gcc ttc agt Phe Phe Lys Tyr Phe Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe Ser 380 385 390 395	1323
ctg att cag gag aac gag gtc ctc ttc acc atg tgc ttc atc ccc ctg Leu Ile Gln Glu Asn Glu Val Leu Phe Thr Met Cys Phe Ile Pro Leu 400 405 410	1371
gtc tgc tgg atc gtg tgc act gga ctg aaa cag cag atg gag agt ggc Val Cys Trp Ile Val Cys Thr Gly Leu Lys Gln Gln Met Glu Ser Gly 415 420 425	1419
aag agc ctt gcc cag aca tct aag acc acc acc gcg gtg tac gtc ttc Lys Ser Leu Ala Gln Thr Ser Lys Thr Thr Thr Ala Val Tyr Val Phe 430 435 440	1467

FIG. 4B

ttc ctt tcc agt ttg ctg cag ccc cgg gga ggg agc cag gag cac ggc	1515
Phe Leu Ser Ser Leu Leu Gln Pro Arg Gly Gly Ser Gln Glu His Gly	
445 450 455	
ctc tgc gcc cac ctc tgg ggg ctc tgc tct ttg gct gca gat gga atc	1563
Leu Cys Ala His Leu Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly Ile	
460 465 470 475	
tgg aac cag aaa atc ctg ttt gag gag tcc gac ctc agg aat cat gga	1611
Trp Asn Gln Lys Ile Leu Phe Glu Glu Ser Asp Leu Arg Asn His Gly	
480 485 490	
ctg cag aag gcg gat gtg tct gct ttc ctg agg atg aac ctg ttc caa	1659
Leu Gln Lys Ala Asp Val Ser Ala Phe Leu Arg Met Asn Leu Phe Gln	
495 500 505	
aag gaa gtg gac tgc gag aag ttc tac agc ttc atc cac atg act ttc	1707
Lys Glu Val Asp Cys Glu Lys Phe Tyr Ser Phe Ile His Met Thr Phe	
510 515 520	
cag gag ttc ttt gcc gcc atg tac tac ctg ctg gaa gag gaa aag gaa	1755
Gln Glu Phe Phe Ala Ala Met Tyr Tyr Leu Leu Glu Glu Glu Lys Glu	
525 530 535	
gga agg acg aac gtt cca ggg agt cgt ttg aag ctt ccc agc cga gac	1803
Gly Arg Thr Asn Val Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg Asp	
540 545 550 555	
gtg aca gtc ctt ctg gaa aac tat ggc aaa ttc gaa aag ggg tat ttg	1851
Val Thr Val Leu Leu Glu Asn Tyr Gly Lys Phe Glu Lys Gly Tyr Leu	
560 565 570	
att ttt gtt gta cgt ttc ctc ttt ggc ctg gta aac cag gag agg acc	1899
Ile Phe Val Val Arg Phe Leu Phe Gly Leu Val Asn Gln Glu Arg Thr	
575 580 585	
tcc tac ttg gag aag aaa tta agt tgc aag atc tct cag caa atc agg	1947
Ser Tyr Leu Glu Lys Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile Arg	
590 595 600	
ctg gag ctg ctg aaa tgg att gaa gtg aaa gcc aaa gct aaa aag ctg	1995
Leu Glu Leu Leu Lys Trp Ile Glu Val Lys Ala Lys Ala Lys Lys Leu	
605 610 615	
cag atc cag ccc agc cag ctg gaa ttg ttc tac tgt ttg tac gag atg	2043
Gln Ile Gln Pro Ser Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu Met	
620 625 630 635	
cag gag gag gac ttc gtg caa agg gcc atg gac tat ttc ccc aag att	2091
Gln Glu Glu Asp Phe Val Gln Arg Ala Met Asp Tyr Phe Pro Lys Ile	
640 645 650	
gag atc aat ctc tcc acc aga atg gac cac atg gtt tct tcc ttt tgc	2139
Glu Ile Asn Leu Ser Thr Arg Met Asp His Met Val Ser Ser Phe Cys	
655 660 665	

FIG. 4C

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

att gag aac tgt cat cgg gtg gag tca ctg tcc ctg ggg ttt ctc cat	2187
Ile Glu Asn Cys His Arg Val Glu Ser Leu Ser Leu Gly Phe Leu His	
670 675 680	
aac atg ccc aag gag gaa gag gag gag gaa aag gaa ggc cga cac ctt	2235
Asn Met Pro Lys Glu Glu Glu Glu Glu Glu Lys Glu Gly Arg His Leu	
685 690 695	
gat atg gtg cag tgt gtc ctc cca agc tcc tct cat gct gcc tgt tct	2283
Asp Met Val Gln Cys Val Leu Pro Ser Ser Ser His Ala Ala Cys Ser	
700 705 710 715	
cat gga ttg gtg aac agc cac ctc act tcc agt ttt tgc cgg ggc ctc	2331
His Gly Leu Val Asn Ser His Leu Thr Ser Ser Phe Cys Arg Gly Leu	
720 725 730	
ttt tca gtt ctg agc acc agc cag agt cta act gaa ttg gac ctc agt	2379
Phe Ser Val Leu Ser Thr Ser Gln Ser Leu Thr Glu Leu Asp Leu Ser	
735 740 745	
gac aat tct ctg ggg gac cca ggg atg aga gtg ttg tgt gaa acg ctc	2427
Asp Asn Ser Leu Gly Asp Pro Gly Met Arg Val Leu Cys Glu Thr Leu	
750 755 760	
cag cat cct ggc tgt aac att cgg aga ttg tgg ttg ggg cgc tgt ggc	2475
Gln His Pro Gly Cys Asn Ile Arg Arg Leu Trp Leu Gly Arg Cys Gly	
765 770 775	
ctc tcg cat gag tgc tgc ttc gac atc tcc ttg gtc ctc agc agc aac	2523
Leu Ser His Glu Cys Cys Phe Asp Ile Ser Leu Val Leu Ser Ser Asn	
780 785 790 795	
cag aag ctg gtg gag ctg gac ctg agt gac aac gcc ctc ggt gac ttc	2571
Gln Lys Leu Val Glu Leu Asp Leu Ser Asp Asn Ala Leu Gly Asp Phe	
800 805 810	
gga atc aga ctt ctg tgt gtg gga ctg aag cac ctg ttg tgc aat ctg	2619
Gly Ile Arg Leu Leu Cys Val Gly Leu Lys His Leu Leu Cys Asn Leu	
815 820 825	
aag aag ctc tgg ttg gtc agc tgc tgc ctc aca tca gca tgt tgt cag	2667
Lys Lys Leu Trp Leu Val Ser Cys Cys Leu Thr Ser Ala Cys Cys Gln	
830 835 840	
gat ctt gca tca gta ttg agc acc agc cat tcc ctg acc aga ctc tat	2715
Asp Leu Ala Ser Val Leu Ser Thr Ser His Ser Leu Thr Arg Leu Tyr	
845 850 855	
gtg ggg gag aat gcc ttg gga gac tca gga gtc gca att tta tgt gaa	2763
Val Gly Glu Asn Ala Leu Gly Asp Ser Gly Val Ala Ile Leu Cys Glu	
860 865 870 875	
aaa gcc aag aat cca cag tgt aac ctg cag aaa ctg ggg ttg gtg aat	2811
Lys Ala Lys Asn Pro Gln Cys Asn Leu Gln Lys Leu Gly Leu Val Asn	
880 885 890	

FIG. 4D

tct ggc ctt acg tca gtc tgt tgt tca gct ttg tcc tcg gta ctc agc	2859
Ser Gly Leu Thr Ser Val Cys Cys Ser Ala Leu Ser Ser Val Leu Ser	
895 900 905	
act aat cag aat ctc acg cac ctt tac ctg cga ggc aac act ctc gga	2907
Thr Asn Gln Asn Leu Thr His Leu Tyr Leu Arg Gly Asn Thr Leu Gly	
910 915 920	
gac aag ggg atc aaa cta ctc tgt gag gga ctc ttg cac ccc gac tgc	2955
Asp Lys Gly Ile Lys Leu Leu Cys Glu Gly Leu Leu His Pro Asp Cys	
925 930 935	
aag ctt cag gtg ttg gaa tta gac aac tgc aac ctc acg tca cac tgc	3003
Lys Leu Gln Val Leu Glu Leu Asp Asn Cys Asn Leu Thr Ser His Cys	
940 945 950 955	
tgc tgg gat ctt tcc aca ctt ctg acc tcc agc cag agc ctg cga aag	3051
Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser Leu Arg Lys	
960 965 970	
ctg agc ctg ggc aac aat gac ctg ggc gac ctg ggg gtc atg atg ttc	3099
Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val Met Met Phe	
975 980 985	
tgt gaa gtg ctg aaa cag cag agc tgc ctc ctg cag aac ctg ggg ttg	3147
Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn Leu Gly Leu	
990 995 1000	
tct gaa atg tat ttc aat tat gag aca aaa agt gcg tta gaa aca ctt	3195
Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr Leu	
1005 1010 1015	
caa gaa gaa aag cct gag ctg acc gtc gtc ttt gag cct tct tgg tag	3243
Gln Glu Glu Lys Pro Glu Leu Thr Val Val Phe Glu Pro Ser Trp *	
1020 1025 1030	
gagtggaaac ggggctgcc aacgccagtg ttctccggtc cctccagctg ggggccctca	3303
ggtggagaga gctgcgatcc atccaggcca agaccacagc tctgtgatcc ttccggtgga	3363
gtgtcggaga agagagcttg ccgacgatgc cttcctgtgc agagcttggg catctccttt	3423
acgccagggt gaggaagaca ccaggacaat gacagcatcg ggtgttggtc tcatcacagc	3483
gcctcagtta gaggatgttc ctcttggtga cctcatgtaa ttagctcatt caataaagca	3543
ctttctttat ttttctcttc tctgtctaac tttctttttc ctatcttttt ttcttctttg	3603
ttctgtttac ttttgctcat atcatcatt ccgctaact tctattaact gaccataaca	3663
cagaactagt tgactatata ttatgttgaa attttatggc agctatttat ttatttaa	3723
tttttgtaat agttttgttt tctaataaga aaaatccatg cttttttag ctggttgaaa	3783
attcaggaat atgtaaaaact ttttggtatt taattaaatt gattcctttt cttaatttta	3843
aaaaaaaaaaaa	3857

FIG. 4E

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

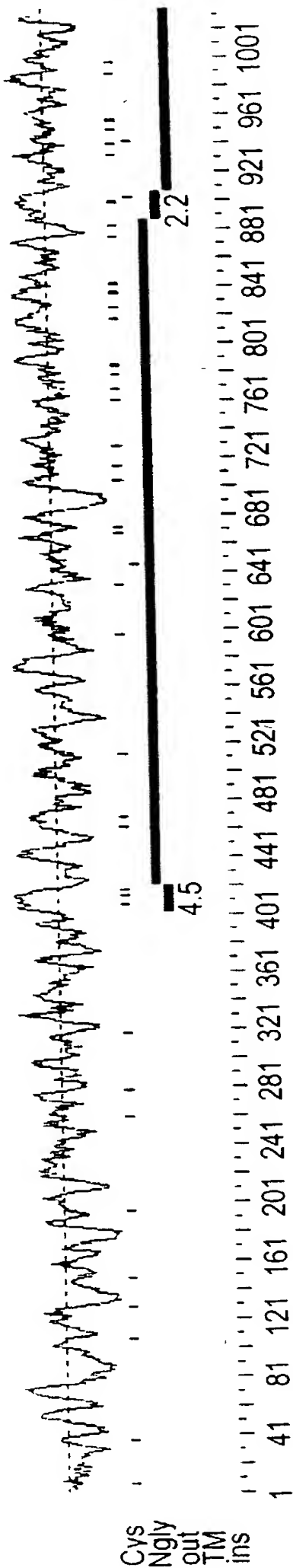
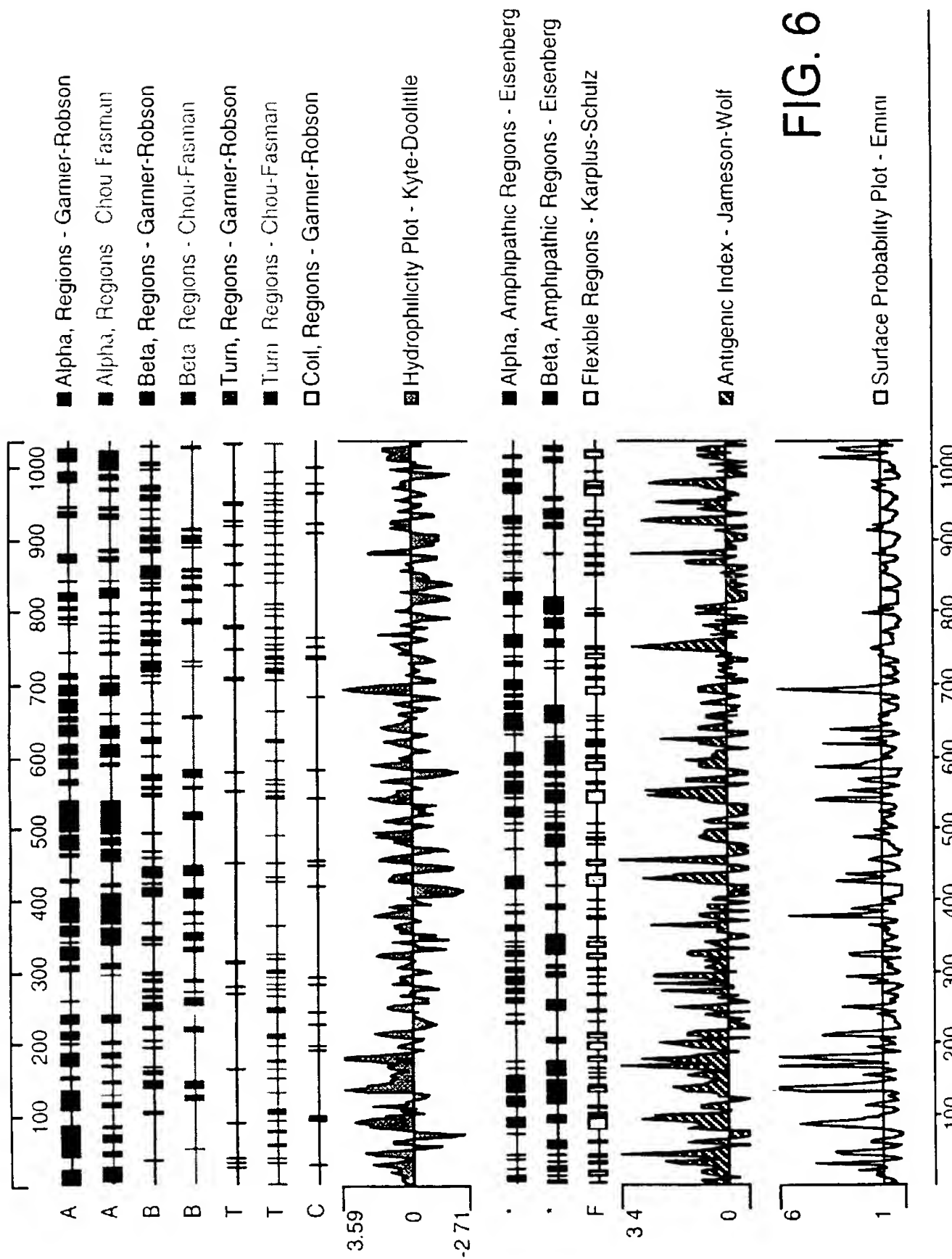


FIG. 5



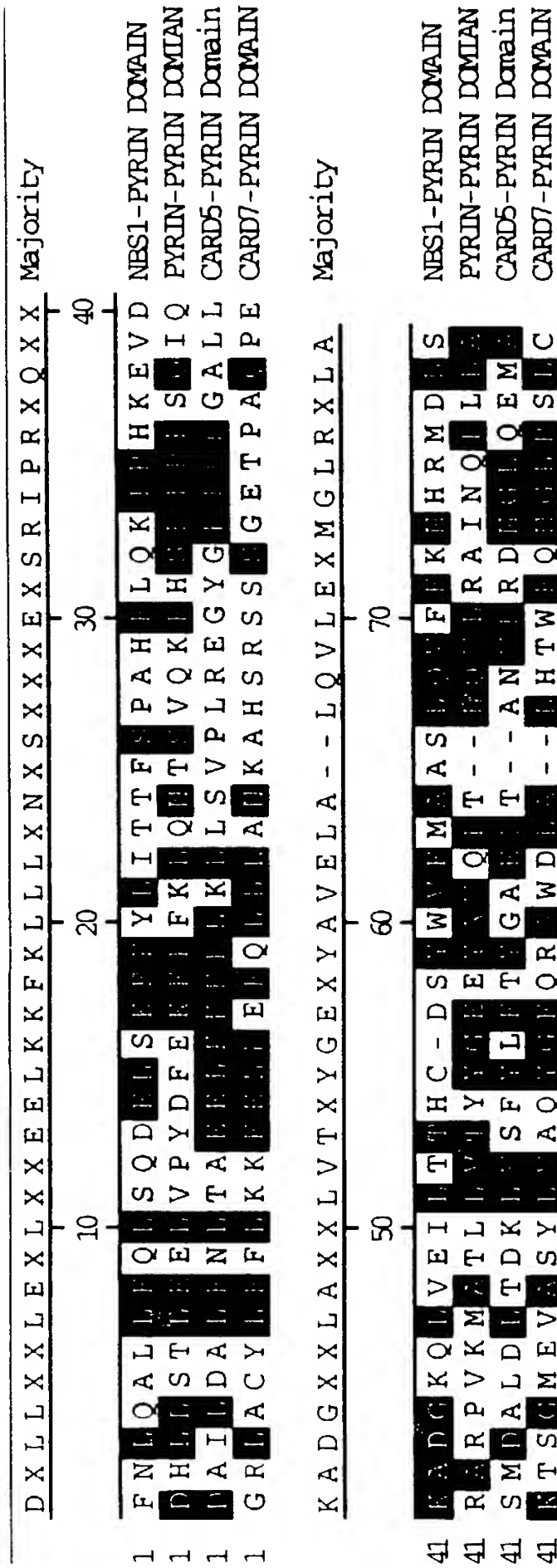


FIG. 7

LRR_RI_2: domain 1 of 8, from 726 to 752: score 0.1, E =
 *->npsLrelLsnNklgdeGaralaealks<.
 *** L L++N+ d+ aL+e+L++
 NBS1 726 HKTVTYLTQGNQ-QDDMFALCEVLRH 752

FIG. 8A

LRR_RI_2: domain 2 of 8, from 782 to 809: score 20.8, E = 0.031
 *->npsLrelLsnNklgdeGaralaealks<.
 n+sL +Ls+N l deGa+ L +L++
 NBS1 782 NQSLTCVNLSDNELLDEGAKLLYTTLRH 809

FIG. 8B

LRR_RI_2: domain 3 of 8, from 811 to 838: score 21.9, E = 0.016
 *->npsLrelLsnNklgdeGaralaealks<.
 ++ L++L+L+n++l+++ ++ La++L
 NBS1 811 KCFLQRLSLENCHLTEANCKDLAAVLVW 838

FIG. 8C

LRR_RI_2: domain 4 of 8, from 839 to 866: score 13.4, E = 0.56

*->npsLreLdLsnNklgdeGaralaealks<--

++ L L L+ N++g G++ L+e+L+

NBS1 839 SRELTHLCLAKNPIGNTGVTGKFLCEGLRY 866

FIG. 8D

LRR_RI_2: domain 5 of 8, from 868 to 895: score 17.0, E = 0.17

*->npsLreLdLsnNklgdeGaralaealks<--

++L++L L+n++++ +G+ L ++L++

NBS1 868 ECKLQTLVLWNCITSDGCCDLTKLLQE 895

FIG. 8E

LRR_RI_2: domain 6 of 8, from 896 to 923: score 22.6, E = 0.0091

*->npsLreLdLsnNklgdeGaralaealks<--

++sL+ LdL+ N++g +G++ L+eal+

NBS1 896 KSSLLCLDLGLNHIGVKGMKFLCEALRK 923

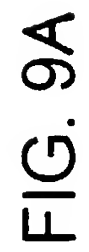
FIG. 8F

LRR_RI_2: domain 7 of 8, from 925 to 952: score 15.8, E = 0.26
-->npsLrøLdLsnNklgdeGaralaealks<--
+++Lr L+L+++ + + L++aL+
NBS1 925 LCNLRCLWLWGCSIPPFSCEDLCSALSN 952

FIG. 8G

LRR_RI_2: domain 8 of 8, from 953 to 979: score 14.0, E = 0.47
-->npsLrøLdLsnNklgdeGaralaealks<--
+sL +LdL++N+lg +G++ L e+L+
NBS1 953 -QSLVTLDLGQNPLGSSGVKMLFETLTC 979

FIG. 8H



NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF

PYPAFI	MAS	TR	CK-	L	AR	YLE	D	L	EDVD	LKKFK	MHL	EDY	P	P	Q	K	G	C	I	P	L	PRGO	TEK	46																
pytin	MAK	TPS	DH	LL	ST	LE	E	L	V	P	YDFE	KFK	F	K	L	QNTSV	Q	K	E	H	SRIPR	S	Q	IQR	47															
CARD7	MAG	GA	WGR	L	AC	YLE	F	L	KK	EELK	E	F	Q	L	L	ANKA	H	S	R	S	S	GETPA	Q	PEK	47															
ASC	MG	RA	R-	DA	I	L	DA	LEN	L	T	A	EELK	K	F	K	L	LS	V	P	L	R	E	G	Y	46															
NBSI	MG	FN	---	L	Q	AL	LE	Q	L	SQD	EL	S	K	F	K	YLIT	T	F	S	P	A	H	E	L	Q	43														
POPI	MG	TK	R-E	A	I	L	KV	LEN	L	I	P	E	L	L	K	F	M	K	L	G	T	V	P	L	R	E	46													
PYPAFI	AD	H	V	D	L	A	T	L	MID	F	N	G	E	E	K	A	W	A	M	A	V	W	I	F	A	A	INR	R	D	L	Y	E	K	A	K	R	D	--EP	90	
pytin	ARP	V	K	M	A	T	L	L	V	T	Y	G	E	E	Y	A	V	Q	L	T	L	Q	V	L	R	A	INQ	R	L	L	A	E	ELH	RA	---	A	90			
CARD7	TS	G	M	E	V	A	S	Y	LVA	Q	Y	G	E	Q	R	A	W	D	L	A	L	H	T	W	E	Q	MGLR	S	L	C	A	Q	A	Q	-E--G	A	90			
ASC	MD	A	L	D	L	T	D	K	LV	S	F	Y	L	E	T	Y	G	A	E	L	TAN	V	L	R	D	MGL	Q	E	M	A	G	Q	L	Q	A	---	T	89		
NBSI	AD	G	K	Q	L	V	E	I	L	T	H	C	D	S	Y	W	V	E	M	A	S	LQV	F	E	K	MHRM	D	L	S	E	R	A	K	D	E	V	R	A	89	
POPI	L	D	I	V	D	L	T	D	K	LVA	S	Y	E	D	Y	A	A	E	L	VVA	V	L	R	D	M	R	M	L	E	E	A	A	R	L	Q	R	A	---	A	89

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the Consensus exactly.

Decoration 'Decoration #3': Box residues that match the Consensus exactly.

FIG. 9B

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

LRR: domain 1 of 9, from 740 to 767: score 10.9, E = 25 FIG. 10A
 ->nLeeLdLsnN.Lt....slppglfsnLp<-
 +L+eLdLs+N+L +++ + +++++
 pyrin-1 740 SLTELDLSDNsLGdpgmRVLCEtLQHPG 767

LRR: domain 2 of 9, from 769 to 796: score 2.3, E = 4.6e+02 FIG. 10B
 ->nLeeLdLsnN.Lt....slppglfsnLp<-
 n+++L+L +++L+++ +++ ++s+ +
 pyrin-1 769 NIRRLWLGRcGLSheccfDISL-VLSSNQ 796

LRR: domain 3 of 9, from 797 to 821: score 9.7, E = 39 FIG. 10C
 ->nLeeLdLsnN.Lt..slppglfsnLp<-
 +L eLdLs+N L + ++ 1+ +L+
 pyrin-1 797 KLVELDLSDNaLGdfGIRL-LCVGLK 821

LRR: domain 4 of 9, from 826 to 849: score 4.1, E = 2.5e+02 FIG. 10D
 ->nLeeLdLsnN.LtslppglfsnLp<-
 nL++L+L ++ Lts +++
 pyrin-1 826 NLKKLWLVSccLTSACCQDLASVL 849

LRR: domain 5 of 9, from 854 to 878: score 0.6, E = 8.2e+02 FIG. 10E
 ->nLeeLdLsnN.Lt..slppglfsnLp<-
 +L++L++ N L ++++ 1+++ +
 pyrin-1 854 SLTRLyVGENaLGdsGVAI-LCEKAK 878

LRR: domain 6 of 9, from 883 to 906: score 5.1, E = 1.8e+02 FIG. 10F
 ->nLeeLdLsnN.LtslppglfsnLp<-
 nL++L L n +Lts+ +++s+
 pyrin-1 883 NLQKLGLVNSgLTSVCCSALSSVL 906

LRR: domain 7 of 9, from 911 to 935: score 10.2, E = 32 FIG. 10G
 ->nLeeLdLsnN.Lt..slppglfsnLp<-
 nL++L+L++N+L ++++ 1+++L
 pyrin-1 911 NLTHLYLRGntLGdkGIKL-LCEGLL 935

LRR: domain 8 of 9, from 940 to 967: score 5.8, E = 1.4e+02 FIG. 10H
 ->nLeeLdLsnN.Lt....slppglfsnLp<-
 +L++L L+n++L++ +l+ 1+ + +
 pyrin-1 940 KLQVLELDNCnLTshccwDLST-LLTSSQ 967

LRR: domain 9 of 9, from 968 to 991: score 8.4, E = 59 FIG. 10I
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L+L nN+L +l f+
 pyrin-1 968 SLRKLSLGNNdLGDLGVMMFCEVL 991

FIG. 11

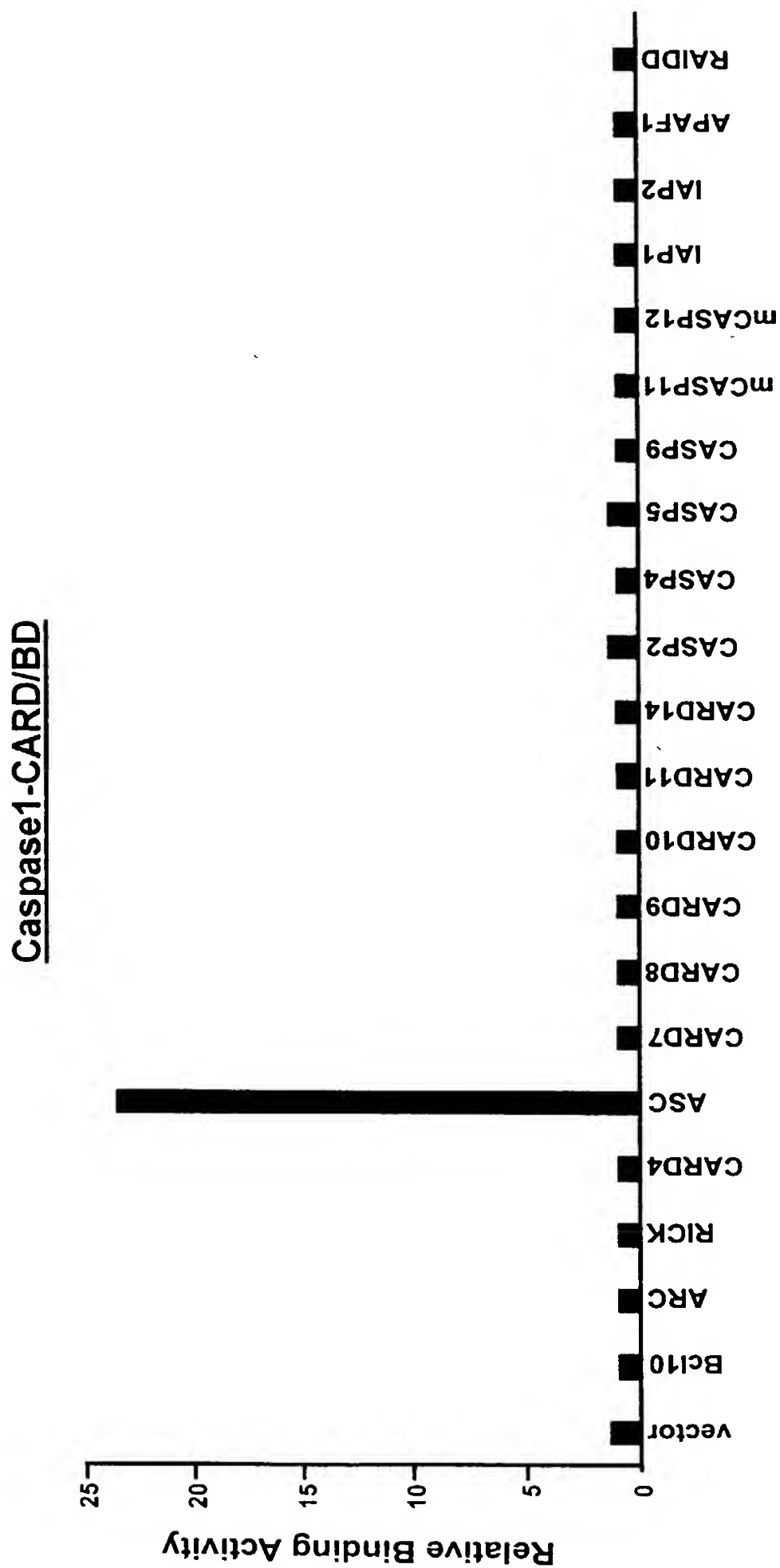


FIG. 12

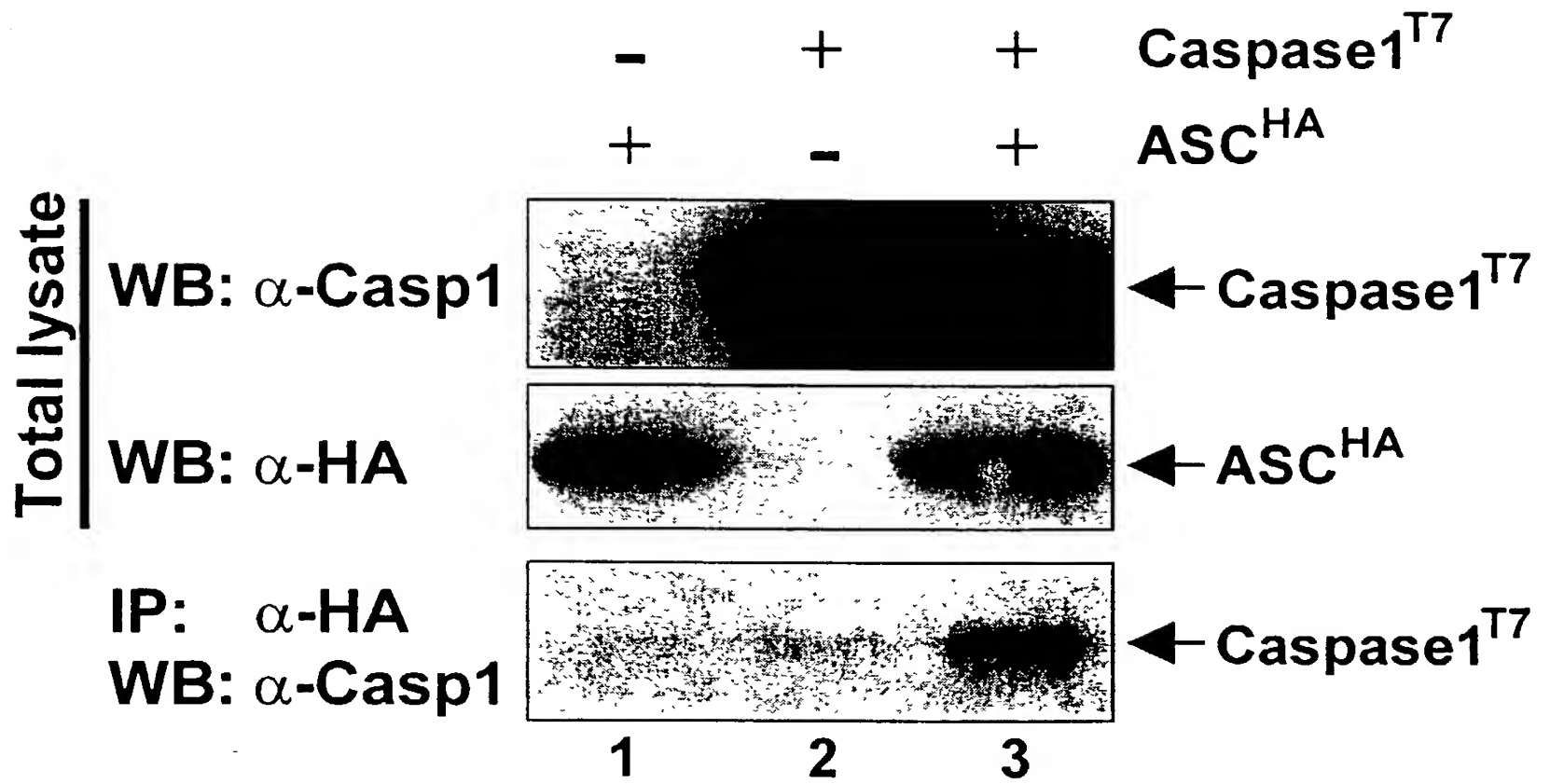


FIG. 13

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF

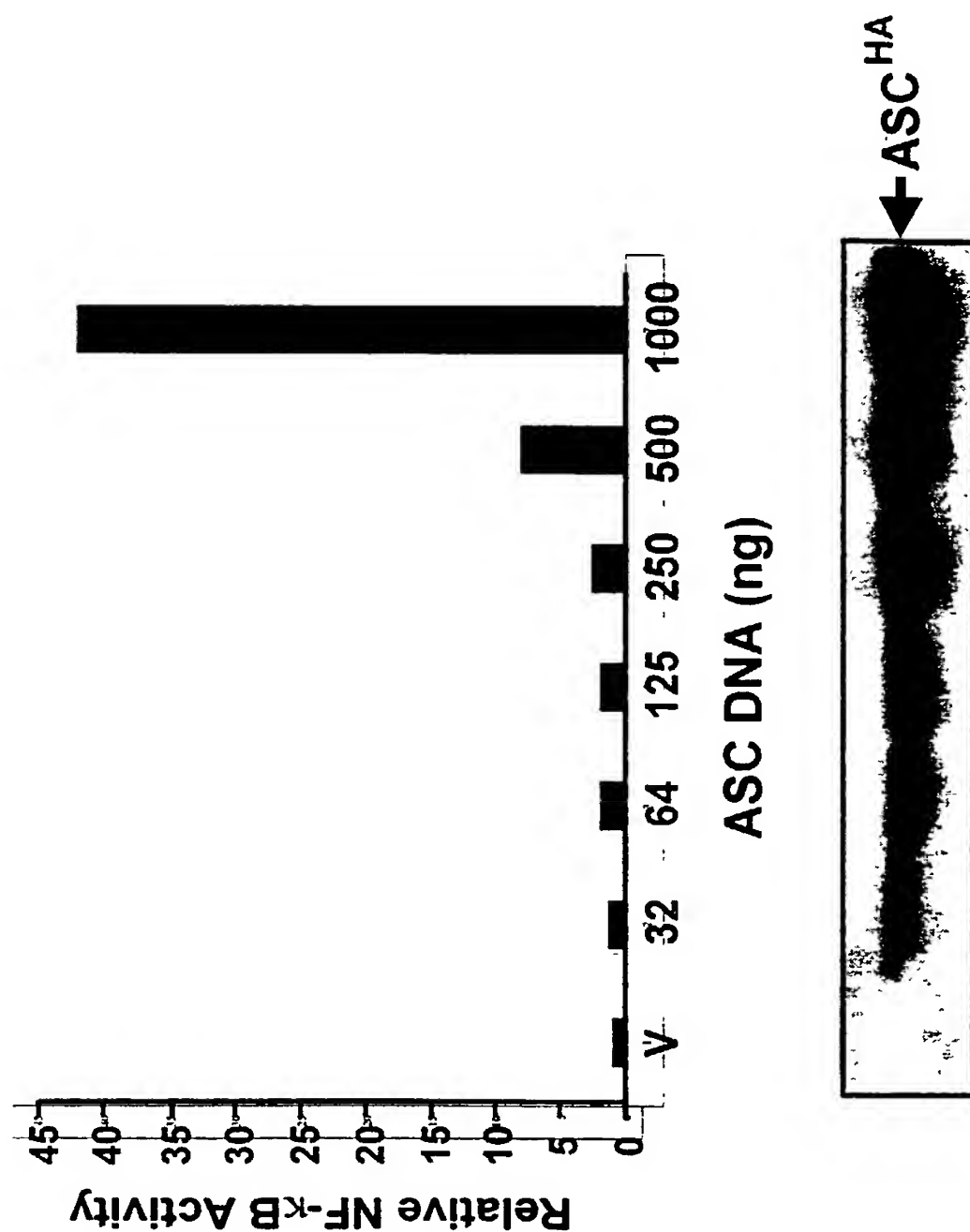


FIG. 14

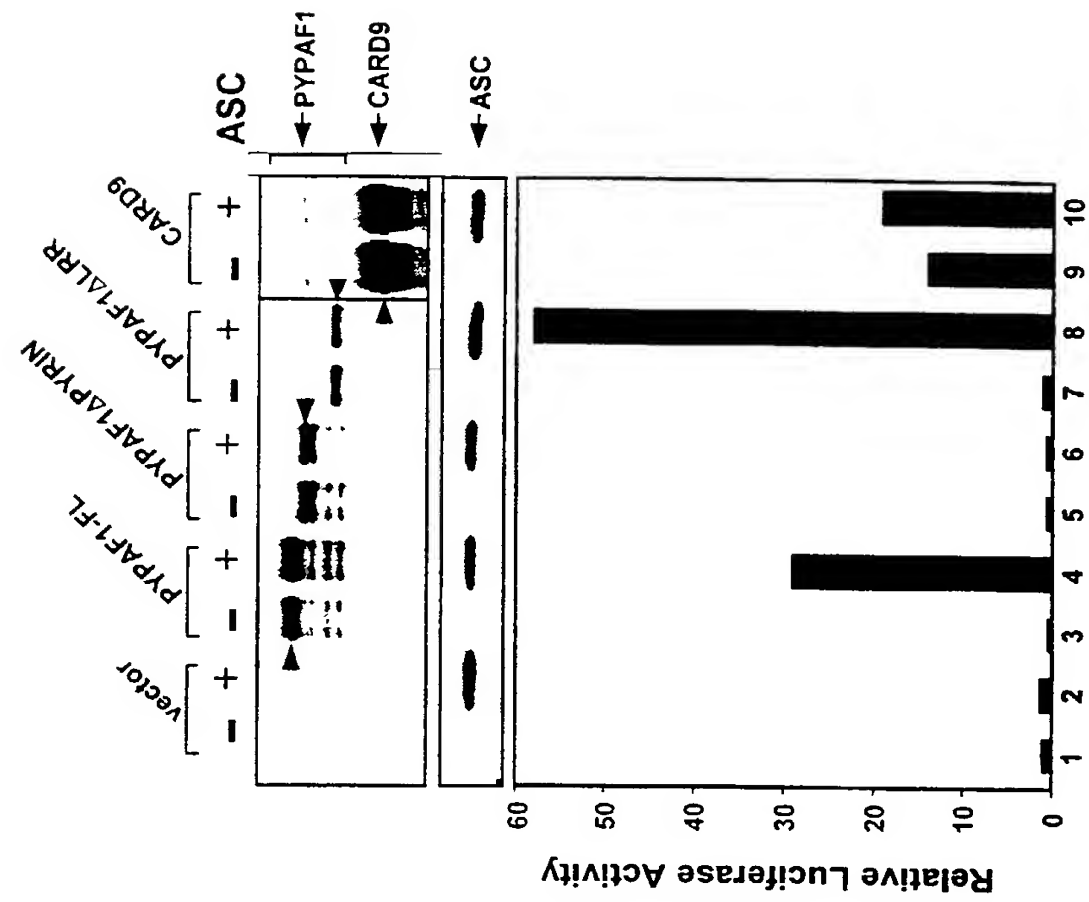


FIG. 15

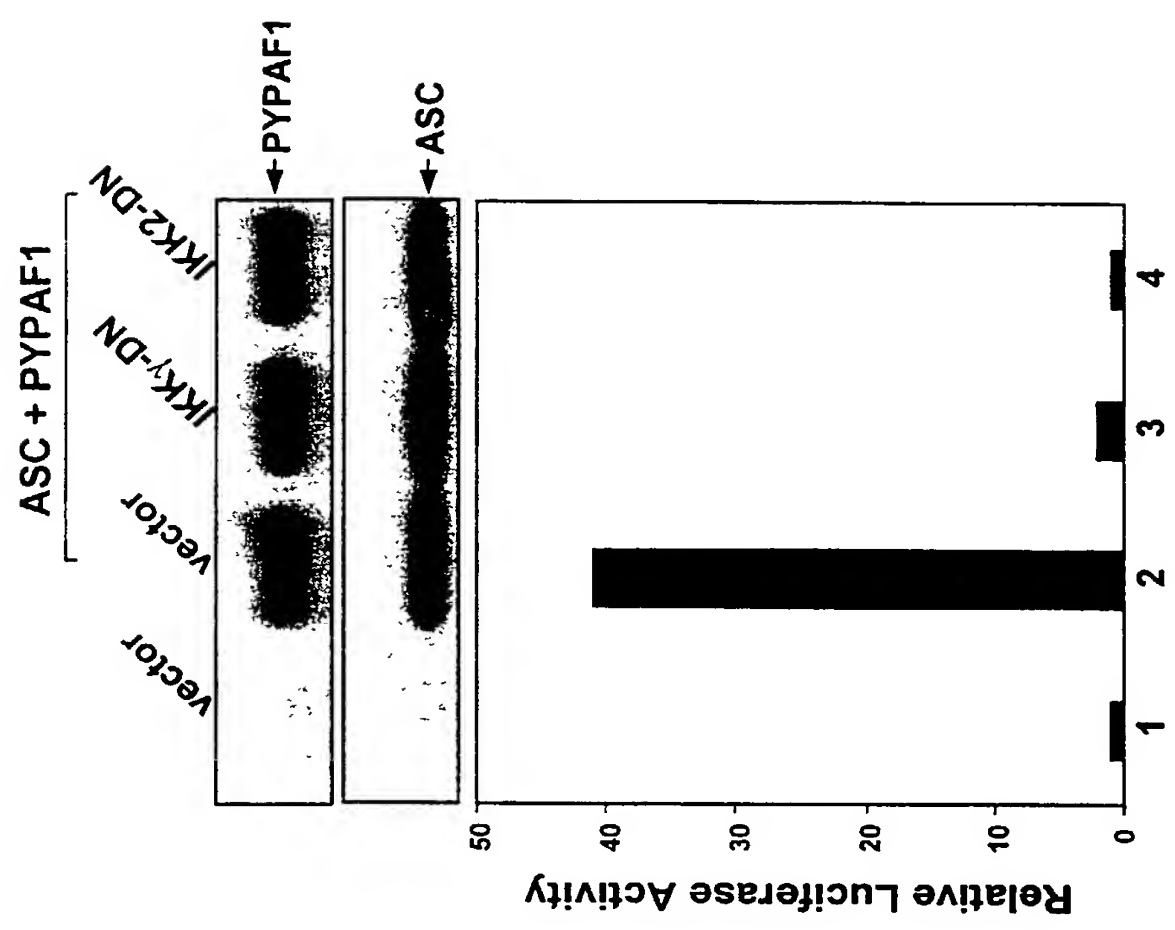


FIG. 16

mPyrin Expression in Normal Mouse Cell Panel



FIG. 17

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
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Pyrin-1 Expression in ABT Model

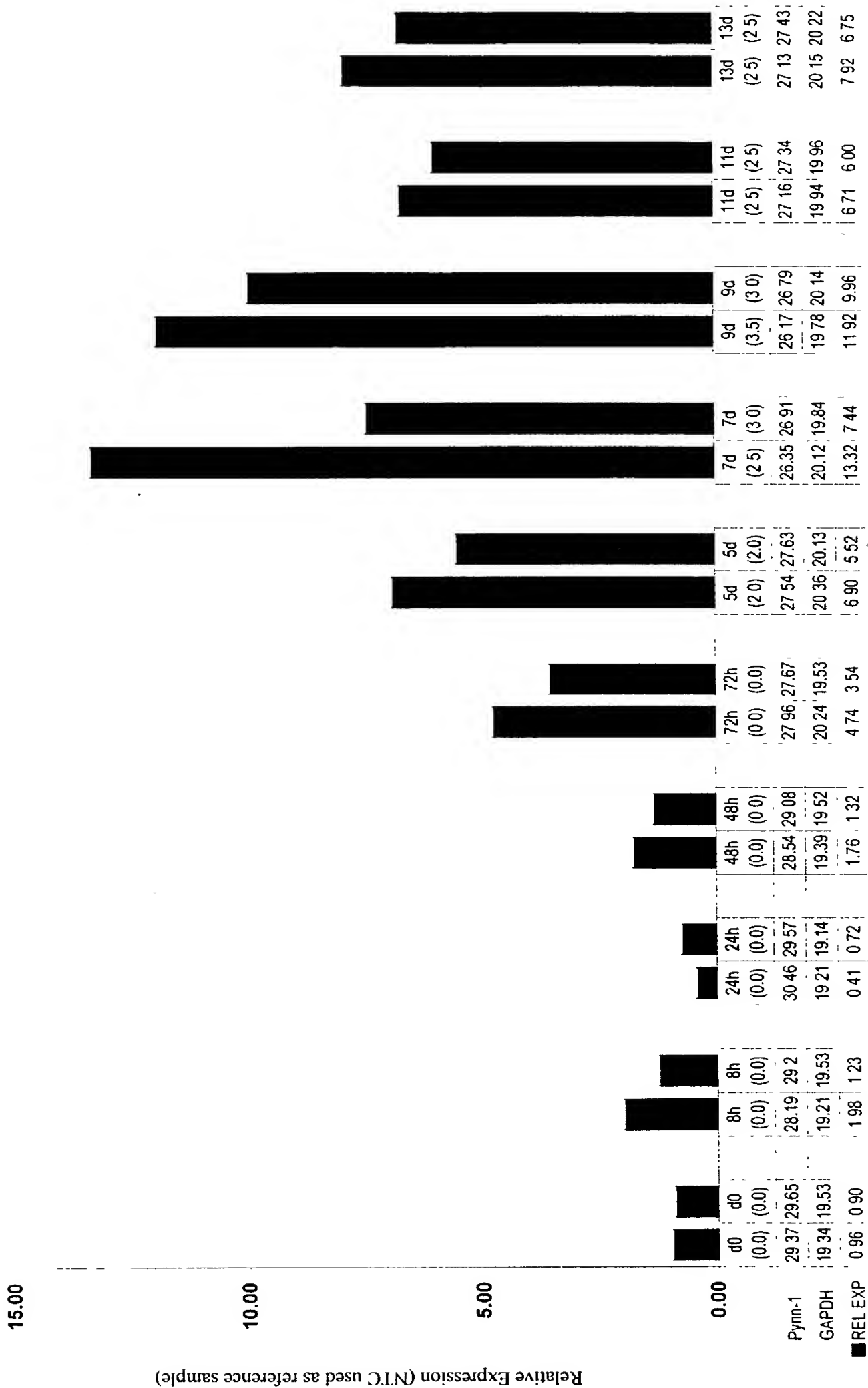


FIG. 18

Pyrin-1 Expression in CIA Model

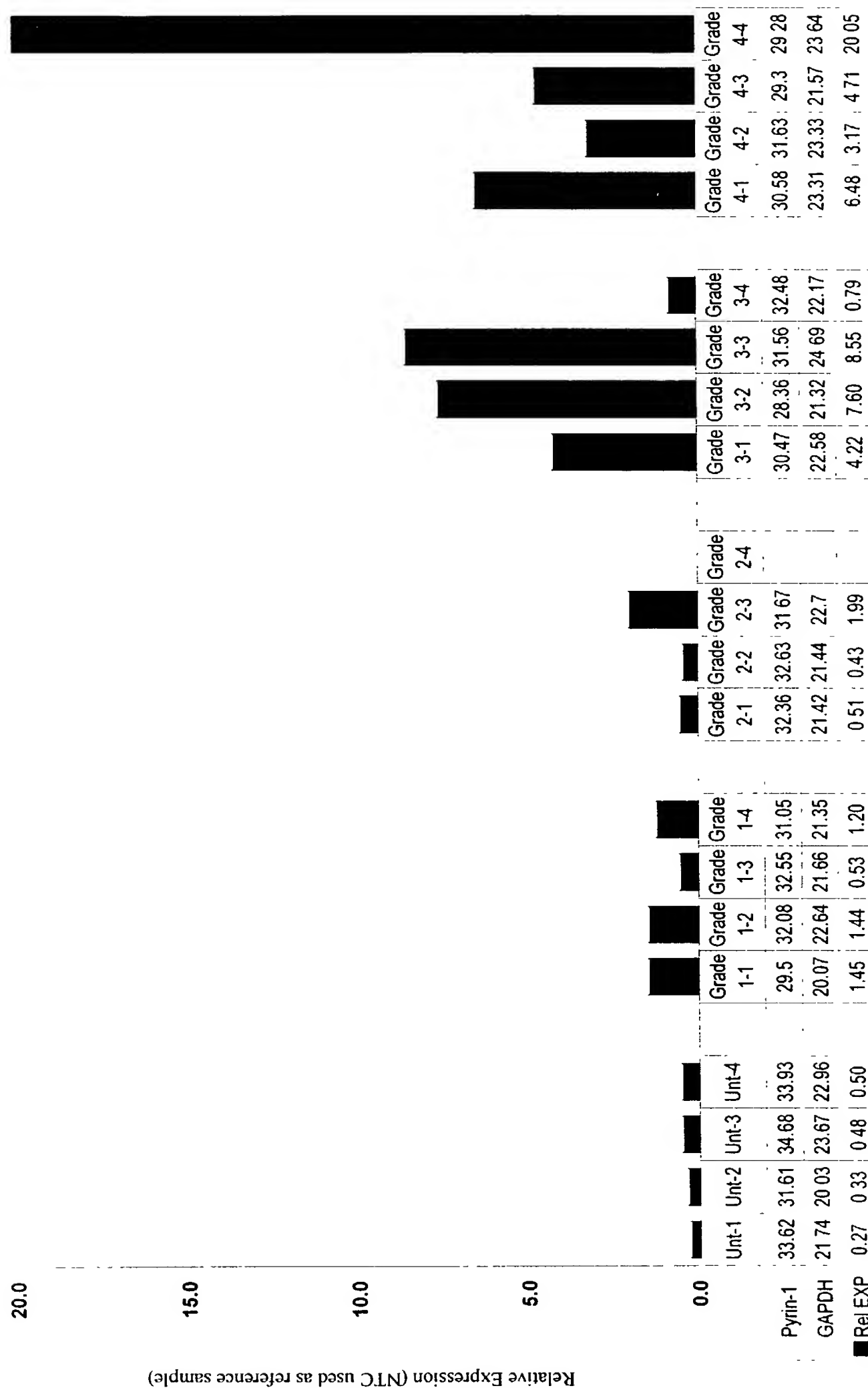


FIG. 19